

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:09 ; Search time 18 Seconds

(without alignments)
1292,474 Million cell updates/sec

Title: US-09-978-309a-74

Perfect score: 1195

Sequence: 1 QEKYDSMVOSLEDVTAQFES.....KKKQSETKLOEELNKVLGIR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1193	99.8	725	1 JC5016	hyaluronan recepto
2	914	76.5	631	2 JC4298	hyaluronan recepto
3	193.5	16.2	955	2 S24348	myosin heavy chain
4	193	16.2	1388	2 T10335	KLP2 protein - Aft
5	191	16.0	1410	1 A57013	early endosome ant
6	190	15.9	1690	2 T13030	microtubule bindin
7	187.5	15.7	741	2 S39082	myosin heavy chain
8	185.5	15.5	1790	2 S67593	transport protein
9	182.5	15.3	1938	2 A59293	skeletal myosin he
10	181.5	15.2	1940	1 A24922	myosin heavy chain
11	179.5	15.0	936	2 S39083	myosin heavy chain
12	179	15.0	697	2 T07111	myosin heavy chain
13	178.5	14.9	1940	1 S04090	myosin heavy chain
14	177.5	14.9	1938	1 JX0178	myosin heavy chain
15	176.5	14.8	845	2 I48176	myosin heavy chain
16	176.5	14.8	1937	2 I38055	synaptonemal compl
17	176.5	14.8	1940	2 A29320	myosin heavy chain
18	175.5	14.7	876	2 A23767	myosin heavy chain
19	175	14.6	993	2 S49461	myosin heavy chain
20	172.5	14.4	439	2 A60608	synaptonemal compl
21	172.5	14.4	864	2 B90395	paramyosin - fluke
22	170	14.2	1388	2 S74245	purine NTPase (imp
23	169	14.1	764	2 S15302	serine/threonine-S
24	169	14.1	1931	2 A59234	myosin heavy chain
25	167	14.0	2245	2 T18278	slow myosin heavy
26	166.5	13.9	1039	2 S18199	myosin heavy chain
27	166	13.9	1300	2 I53799	myosin heavy chain
28	166	13.9	1356	2 S32763	Cg1 protein - huma
29	165	13.8	3187	2 JC5837	kinecltin 1 - human 364k Golgi complex

30	162.5	13.6	1164	2 T24806	hypothetical prote
31	162.5	13.6	1938	2 I49464	alpha cardiac myos
32	162	13.6	1935	2 A59286	myosin heavy chain
33	161.5	13.5	911	2 S51441	hypothetical prote
34	161.5	13.5	1938	1 S06005	myosin alpha heavy
35	161.5	13.5	1939	2 I48175	myosin heavy chain
36	161	13.5	746	2 T47237	myosin II heavy ch
37	161	13.5	1935	2 A37102	myosin beta heavy
38	160.5	13.4	4574	2 G02520	plectin - human
39	160	13.4	1679	2 S48385	hypothetical prote
40	160	13.4	1738	2 T14867	interactin - slime
41	160	13.4	1935	1 S06006	myosin beta heavy
42	160	13.4	1979	1 S03166	myosin heavy chain
43	159.5	13.3	1597	2 S68420	clitron - mouse
44	158	13.2	978	2 A70387	conserved hypothet
45	158	13.2	1156	2 B70356	chromosome assemb

ALIGNMENTS

RESULT 1

JC5016

hyaluronan receptor - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 29-Sep-1999

C:Accession: JC5016

R:Wang, C.; Entwistle, J.; Hou, G.; Li, Q.; Turley, E.A.

Gene 174, 299-306, 1996

A:Title: The characterization of a human RHAMM cDNA: Conservation of the hyaluronan-b

A:Reference number: JC5016; MIM:683209; PMID:8890751

A:Contents: breast

A:Accession: JC5016

A:Molecule type: mRNA

A:Residues: 1-725 <MAN>

A:Cross-references: GB:U29343

A:Note: It is uncertain whether Met-1 or Met-196 is the initiator

C:Comment: This receptor regulates focal adhesion turnover, and regulates human breas

C:Genetics:

A:Gene: GDB:HMNR: RHAMM

A:Cross-references: GDB:683209; OMIM:600936

A:Map position: 5q33.2-3qter

C:Superfamily: hyaluronan receptor

Query Match 99.8%; Score 1193; DB 1; Length 725;

Best local similarity 99.6%; Pred. No. 1.8e-53;

Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	QEKYDSMVOSLEDVTAQFESYKALTAETEDKLENSLSQEKAKAGKNAEDVHOQIAT	60
DB	443	QEKYDSMVOSLEDVTAQFESYKALTAETEDKLENSLSQEKAKAGKNAEDVHOQIAT	502
QY	61	ESSNOEYVAMLDLDTKSAKTEKETVSLQKTTDQNLKQOEEFRQLDEEGR	120
DB	503	ESSNOEYVAMLDLDTKSAKTEKETVSLQKTTDQNLKQOEEFRQLDEEGR	562
QY	121	KAKEENTTAELTEETINKRLLYEELYNKTKPQIOLDAFEVSKQALLNEHGAQPOLNKI	180
DB	563	KAKEENTTAELTEETINKRLLYEELYNKTKPQIOLDAFEVSKQALLNEHGAQPOLNKI	622
QY	181	RDSYAKLLGHONLKOKIRHVYKLDKENSQKSEVSKLRQAKKKQSETKLOEELNKVLG	240
DB	623	RDSYAKLLGHONLKOKIRHVYKLDKENSQKSEVSKLRQAKKKQSETKLOEELNKVLG	682
QY	241	IK 242	
DB	683	IK 684	

RESULT 2

JC4298

hyaluronan receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 01-Dec-2000
C:Accession: J04298; A42925; A41923; S21586
R:Entrez: J. Zhang, S. Yang, B. Wong, C. Li, Q. Hall, C.L., A. J. Mowat, M. G.

Gene 163, 233-238, 1995
A:Title: Characterization of the murine gene encoding the hyaluronan receptor RHAMM.

A:Reference number: J04298; MUID:96011639; PMID:7590272
A:Accession: J04298
A:Molecule type: mRNA

A:Residues: 1-631 <ENT>
A:Cross-references: EMBL:X64550

R:Hardwick, C.
A:Experimental source: 3T3 fibroblast

J. Cell Biol. 118, 753, 1992
A:Reference number: A42925; MUID:92348516; PMID:1639856

A:Contents: extratum
A:Accession: A42925

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-631 <HAN>
A:Cross-references: GB:X64550

R:Hardwick, C.; Hoare, K.; Owens, R.; Hohn, H.P.; Hook, M.; Moore, D.; Clipp, V.; Auste

J. Cell Biol. 117, 1343-1350, 1992
A:Title: Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility

A:Reference number: A41923; MUID:92299690; PMID:1376732
A:Accession: A41923

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-507, 'L', 508-630 <HAN2>
A:Cross-references: GB:X64550

C:Comment: this sequence has been corrected in reference A42925
A:Note: This protein regulates cell motility and transformation, and focal adhesion

A:Gene: rhnm

A:Initons: 20/3; 54/2; 79/2; 137/3; 187/3; 259/2; 382/2; 431/2; 482/2; 515/3; 574/3; 625
C:Superfamily: hyaluronan receptor

F:260-382/Region: 21 residue repeats
F:516-574/Region: hyaluronan binding #status predicted

F:575-625/Region: hyaluronan binding #status predicted
F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (asn) (covalent) #status

Query Match
Best Local Similarity 76.5%; Score 914; DB 2; Length 631;

Matches 184; Conservative 20; Mismatches 38; Indels 0; Gaps 0;

QY 1 QEKDMSVQSELEVTAFESYKALTAETEDLKLENSLOEKAKNAEDVOHQIAT 60

DB 363 QEKNDPAOSLRDVTALQLESYSSTLEKEDLKLENTLQEKVAAEKSVEDVOQIITA 422

QY 61 ESSNOEYVRLDLQTSALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGR 120

DB 423 ESTNOEYVRLDLQTSALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGR 120

QY 121 KAEKETVAFELTEELNKRLYEELYNKTPFOQLDAFEVEKQALLNEGAQOELMTI 180

DB 483 TAEKENVMTLEMTENKRLLYDELTEKTPFOQLDAFEVEKQALLNEGAQOELMTI 180

QY 181 RDSYAKLLGHONLKOKIKHVKLKDENSOLKSEVSKIRCOLAKKOSKTLDEELNKVIG 240

DB 543 RDSYAKLLGHONLKOKIKHVKLKDENSOLKSEVSKIRCOLAKKOSKTLDEELNKVIG 240

QY 241 IR 242

DB 603 IR 604

RESULT 3
S24348
myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment
C:Species: Gallus gallus (chicken)
C:Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C:Accession: S24348

R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform

A:Reference number: S24348; MUID:92309413; PMID:1377278
A:Accession: S24348

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-955 <MOO>
A:Cross-references: EMBL:M74085

C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP, coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match
Best Local Similarity 16.2%; Score 193.5; DB 2; Length 955;

Matches 76; Conservative 53; Mismatches 106; Indels 121; Gaps 9;

QY 8 VQSELEVTAFESYKALTAETEDLKLENSLOEKAKNAEDVOHQIATESNOEY 67

DB 226 IDNLRVQKQLEKSEKLEMEITDILASNNSEYKAKANLEKCRILEQLSKIRKEEH 285

QY 68 VRMLDLQTSALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGR 120

DB 286 QRMINDLSTQRAQLQTSALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGR 120

QY 107 -----EED-----FRKQLEDEGRKAEKENTTAETELTEINKRLLY-----EEL 145

DB 346 NALNALQSARDCCLLAEQYEEDQKAGELQRAKSNSEVQAKRYETDIAIQTTEL 405

QY 146 YAKTTPFOQLD-----AFVEKQALLNE-----HGAQOELNKRIR 181

DB 406 EAKKRIALQRLQDAEHEVAVNACASLETKQRLQNEVEDLMIDVERANACARLDKQ 465

QY 182 DSYAKLLGHONLKOKIKHVKLKDENSOLKSEVSKIRCOLAKKOSKTLDEELNKVIG 240

DB 466 KNFKKILAEKQKYEELQALQESRSLSSTLEFKMNAVEESDLHLETKRNNKIQ 525

QY 212 SEVSKLQCLAK-----KQ-----SETKQLEELNVLGIR 242

DB 526 QEISDLEQIAEGKAIHLEKVKQIQEKEISQALAEVASELHEGKIRLQ 581

RESULT 4
T30335

KLP2 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 02-Jun-2000
C:Accession: T30335

R:Bolet, H.; Karsenti, E.; Veinos, I.
Cell 84, 49-59, 1996

A:Title: Klp2, a new Xenopus centrosomal kinesin-like protein required for centrosom

A:Reference number: 220827; MUID:96140639; PMID:8548825
A:Accession: T30335

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-1388 <BO>
A:Cross-references: EMBL:X34082; NID:91129172; PID:6213754; PIDN:CAA63826.1

C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology

Query Match
Best Local Similarity 16.2%; Score 193; DB 2; Length 1388;

Matches 71; Conservative 51; Mismatches 92; Indels 96; Gaps 7;

QY 9 QSELEVTAFESYKALTAETEDLKLENSLOEKAKNAEDVOHQIATESNOEY 67

DB 1079 EELKTEAFKQKQALLHTEKELVEKQISLTQVQKIMLDTLETSRQKIRASNS 1138

QY 51 -----EDVOHQIATE-----SSNOEYVRLDLQTSALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGR 120

DB 1139 SSPVLPETPRTEGPNPYSEIANLQKRNMTNLEIVSELNERTKNEITRL-----K 1192

QY 78 SALKETKEITVSLQITDLOQLQOEEDPFKOLEDEGRK 122

RESULT 6

A:Accession: A30170
A:Reference number: A30170; MUID:89210285; PMID:2707122

QY	5	DSMVQSLSDVDAQFESYKALNTAS	-----	FIEDPLKLENSLQKAKKAGNAADYQHOI	57				
Db	1148	ESLEKEHDDLAQAKTIEQJANKEROYNEEISQINDLITSTQOENESIKKKNDELBEV	1207						
QY	58	LATESSNOEYVRM	-----	LIDLQTSALKETEIKETIV	-----	SFLQKITDLONOI	103		
Db	1208	KAMSTSEOSNLKKSSEIDALNLOIKELKKNENNEASLLESIKSVSEYVKKIKELQDEC	1267						
QY	104	KQOEDEFKQLEDEGRKAEKENTTAELTEELINKWRLLYELNKKRPFQQLDAF	-----	159					
Db	1268	NFKEREV-SELEDKTKASEDNKSYLELOKSEK	-----	IKRELDKATTELKLTQLEKTNLS	1323				
QY	160	-----EYE	-----	KQALINENGAQEOELNKR	-----	DSYAKLIGH	-----	QNL	193
Db	1324	KAKKSESELSRLKKTTSSEKKNAPQOLEKLNKNIQIKNQAFERKRLNNGSSITIOEY	1383						
QY	194	KQKTK	-----	HHVTKLKDENSQLSKSEVSKRLCOLAKKQSETKLOE	234				
Db	1384	SEKINTLEDELIRLOENENELKAKEIDWTRSELEKVSINDLEEE	1428						

RESULT 9

A599293

skeletal myosin heavy chain - domestic rabbit

C:Species: Oryctolagus cuniculus

C:Date: 09-Jun-2000 #sequence

C:Revision: 09-Jun-2000 #text_change 08-Sep-2000

C:Accession: A599293

R:Maeda, K.; Hostinova, E.; Rossc, Kleinkauf, A.; Schuster, H.; Gasperi, J.; Wittingh

submitted to Genbank, July 1995

A:Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal

A:Reference number: A599293

A:Accession: A599293

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1938 <MAE>

A:Cross-references: GB:032574; NID:g940222; PIDN:AAA74199.1; PID:g940233

A:Experimental source: strain New Zealand White; cell type skeletal muscle fiber type

C:Genetics:

A:Gene: MHC

C:Superfamily: myosin heavy chain; myosin motor domain homology

F:89-769/Domain: myosin motor domain homology <MMO>

QY	8	VOSLIEDVTAQFESYKALNTASEIEDLKLENSLQKAKKAGNAE	-----	DVOHOLITSS	63		
Db	1210	IDNLOKVKQKLEKESLKKKEIDDL	-----	ASNMETVSKAKGNLEKKCRILEDQVSELKTR	1265		
QY	64	NOEYVRMLDLQTSALKETEIKET	-----	VSEFLQKITDLONOI	106		
Db	1266	EEEHORLINDLSQARARLQTESESEFSROLDEKDSIVLSQSRGQAFQTOOLELKLQLEEB	1325				
QY	107	-----EED	-----	FRKQLEDEGRKAEKENTTAELTEELINKWRLLY	-----	142	
Db	1326	IKAKSALAHALQSRHDCDLRQOYEEDEKAKELQPRANSKANSEVAOWMTRKETETDAIOR	1385				
QY	143	BEIYVKKTRPFQQLD	-----	AFVEVQALINE	-----	HGAQEOQL	177

Db 1386 TELLEKKKLAORLODAEEHVAVNAKCAASLEKTKORLONEVEDLMIDVERTNACAAL 1445
QY 178 NKIRDSYAKLLG-----HONLKO-----KIKHYVK-----LKDN 207
Db 1446 DKQORNFDRKLAEMKHKHYETHEALFASOKESRSLSTEYKVKVNAEESIDOLETKREN 1505
QY 208 SOKSEVSKRLCOLAR-----KQO-----SETKLOEELNKVIGIK 242
Db 1506 KNLQOEISDLTEQIAEGGRHIELEKVKROVEQEKSELQALFEAEASLEHEGKILRIQ 1565

RESULT 10

A24922 myosin heavy chain, skeletal muscle, embryonic - rat

N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Apr-2002

C:Accession: A24922; A22538; B24263

R:Strehler, E.E.; Strehler-Page, M.A.; Perltard, J.C.; Perltasamy, M.; Nadal-Ginard, B.

J. Mol. Biol. 190, 291-317, 1986

A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy

A:Reference number: A24922; MWID:87060988; PMID:3783701

A:Accession: A24922

A:Molecule type: DNA

A:Residues: 1-1940 <STR>

A:Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:g1619328

R:Strehler, E.E.; Mahdavi, V.; Perltasamy, M.; Nadal-Ginard, B.

J. Biol. Chem. 260, 468-471, 1985

A:Title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes

A:Reference number: A22538; MWID:85080119; PMID:2981212

A:Accession: A22538

A:Molecule type: DNA

A:Residues: 1-168 <ST2>

A:Cross-references: GB:I00370; GB:M10135; NID:9205580; PIDN:AAA1655.1; PID:9554476

R:Perltasamy, M.; Wydro, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.

J. Biol. Chem. 260, 15856-15862, 1985

A:Title: Characterization of cDNA and genomic sequences corresponding to an embryonic my

A:Reference number: A24263; MWID:86059474; PMID:2999140

A:Accession: B24263

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1358-1490, 'G', <PER>

A:Cross-references: GB:X03468; NID:9205573; PIDN:AAA1652.1; PID:9205574

A:Experimental source: clone PMHC-72

C:Genetics:

A:Introns: 68/3; 116/3; 169/1

A:Note: the list of intron positions may be incomplete

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co

F:89-767/Domain: myosin motor domain homology <MMOT>

F:179-186/Region: nucleotide-binding motif A (P-loop)

F:549-586/Region: actin binding #status predicted

F:656-678/Region: actin binding #status predicted

F:840-1940/Domain: coiled coil #status predicted <COI>

F:840-1280/Region: S2

F:1281-1940/Region: light meromyosin

F:130/Modified site: N6, N6-trimethyllysine (Lys) #status predicted

F:185/Binding site: ATP (Lys) #status predicted

F:696,706/Active site: Cys #status predicted

Query Match

Best Local Similarity 15.2%; Score 181.5; DB 1; Length 1940;

Matches 69; Conservative 62; Mismatches 104; Indels 121; Gaps 7;

QY 8 VOSLEDVTAOFESYKALTASEIEDLKLENSLOEFAAKGNAEDVOHOIILATESSNOY 67

Db 1208 IDNLRVOKLEKSEKLEIDDLSSSEVSYSKKNLEKICRLEEDLSARGKNEET 1267

QY 68 VMLLDLTKSALKEITKEIT-----VSFLQKITDLOLQKOED- 109

Db 1268 ORSISELTQSRLOTEAGEISROLEKESIVSOLSRKQAFQTOIEELKROLEENAK 1327

QY 110 -----FRKLODEEGRAKAKENTTAELTEINKRLLVE----- 143
Db 1328 NALHALQSRHODLLREQEYEEQEGKAELOALRSANSQVAMQRTKYTTDAIQRTTEL 1387
QY 144 -----ELYN-----KTK----- 150
Db 1388 EEAARKKLAORLODSEQEVAVNAKCAASLEKTKORLOGEVEDLWVDERANSIAALDKQ 1447
QY 151 -----PROIOLDAFEVEKQALLNPHGAQOLNKRISYAKLLG-----HONK 194
Db 1448 RNFQVLAEMKTKCEESQALBALKESRSLSTELFKVAYEALDQLETVYKRENNLE 1507
QY 195 QKIKHVVKIKDENSOLKSEVSKRLCOLAKK-----QSEKLOEELNKVIGIK 242
Db 1508 QEIADLTQIAENKRSIHELEKSRQWELKADIQVLAEEAALHEEAKILRIQ 1563

RESULT 11

S39083 myosin heavy chain, neonatal (similarity) - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 03-Feb-1994 #sequence, revision 03-Feb-1994 #text, change 20-Jun-2000

C:Accession: S39083; S24350; A26821

R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

submitted to the EMBL Data Library, August 1991

A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o

A:Reference number: S39081

A:Accession: S39083

A:Molecule type: mRNA

A:Residues: 1-936 <MOO1>

A:Cross-references: EMBL:M74087

R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

J. Mol. Biol. 225, 1143-1151, 1992

A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of iso

A:Reference number: S24348; MWID:92309413; PMID:1377278

A:Accession: S24350

A:Molecule type: mRNA

A:Residues: 3-466, 'Q', 468-641, 'R', 643-936 <MOO2>

A:Cross-references: EMBL:M74087

R:Morality, D.M.; Barringer, K.J.; Dodgson, J.B.; Richter, H.E.; Young, R.B.

DNA 6, 91-99, 1987

A:Title: Genomic clones encoding chicken myosin heavy-chain genes.

A:Reference number: A26821; MWID:87217964; PMID:3034534

A:Accession: A26821

A:Molecule type: DNA

A:Residues: 'F', 856-936 <MO>

A:Cross-references: GB:M1657; NID:9212371; PIDN:AAA48970.1; PID:9212372

C:Genetics:

A:Introns: 886/3

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match

Best Local Similarity 15.0%; Score 179.5; DB 2; Length 936;

Matches 75; Conservative 55; Mismatches 105; Indels 121; Gaps 11;

QY 8 VOSLEDVTAOFESYKALTASEIEDLKLENSLOEFAAKGNAEDVOHOIILATESSNOY 67

Db 208 IDNLRVOKLEKSEKLEIDDLSSSEVSYSKKNLEKICRLEEDLSARGKNEET 267

QY 68 VMLLDLTKSALKEITKEIT-----VSFLQKITDLOLQKOED- 106

Db 268 QMINDVNAORARLQTESEGEYSROYEKKALISOLSRKQAFQTOIEELKRLHEERIK 327

QY 107 -----EED-----FRKLODEEGRAKAKENTTAELTEINKRLLY-----EEL 145

Db 328 NALAGLOSARHODLLREQEYEEQEGKAELOALRSANSQVAMQRTKYTTDAIQRTTEL 387

QY 146 YNKRTPFOQLD-----AFEEVQALNE-----HGAQOELNKR 181

Db 388 EEAARKKLAORLODAEEHVAVNAKCAASLEKTKORLONEVEDLMIDVERANSACALDKQ 447

QY 162 DSYAKVLGHNK-----QKIKHYVKIKDENSOLK 211

Db 448 KNDKILSEWKKYEEFTQAELEASQKESRSLSTELFKMKNAVEESJDHETLRENNKQ 507
 QY 212 SEVSKIRCOLAK-----KKO-----SEFKLOEELNKVGLIK 242
 Db 508 QETSLDTELOAEGKAIHELEKVKQJOEDKESKLSLEAEASLEHEEGKILRLQ 563

RESULT 12

T07111
 MAR binding filament-like protein 1 - tomato

N:Alternate names: MFPI protein

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000

C:Accession: T07111

R:Meier, I.; Phelan, T.; Guissem, W.; Spiker, S.; Schneider, D.

Plant Cell 8, 2105-2115, 1996

A:Title: MFPI a novel plant filament-like protein with affinity for matrix attachment re

A:Reference number: 215928; PMID:97112038; PMID:8953774

A:Accession: T07111

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-697 <MBL>

A:Cross-references: EMBL:X07861; NID:91771157; PIDN:CAA69181.1; PID:91771158

A:Experimental source: strain VFMT Cherry; young fruit

C:Genetics:

A:Gene: MFPI

C:Superfamily: hyaluronan receptor

C:Keywords: DNA binding; nuclear matrix

Query Match

Best Local Similarity 15.0%; Score 179; DB 2; Length 697;

Matches 72; Conservative 57; Mismatches 96; Indels 56; Gaps 12;

QY 1 QEYDSMVSLEVTQAFESYKALIAS-----EIDDLKLENSLOEKAKKNAEDVOH-- 55
 Db 427 QESLENSRSEVSDITVQLDQLRLSKLESEVSKLQME--LETRASLORNIDETKHS 483
 QY 56 QILATE-----SSNOEYVRLMLDLOTKSALKETEKEIVSELOKTTDLONOLOKQ 106
 Db 484 ELIAALITTKELTKLTNEEMHTMSDELVAVSNNRSLOTEL-VNYYKKREHTRNEKQ 542
 QY 107 -----EEDFRKQLEDEGRKAKEKNTALTEELINKMPL-LYEEL 145
 Db 543 KTVITLLEELKFLFSQITREKELRSLEDE--LEK--AVESLDEIRNVLALEEL 595
 QY 146 YNKTFRQIOLDAFEYKQALNEHGAQOLNKINDSTAKL-----GHONLKOKIKHYV 201
 Db 596 ELATSNSSLDEEREVHRQSVSQKQISOEAQENLEDASHLVKLGKRESLEKRAK-- 652
 QY 202 KLDENSOLKSEVSKIRCOLAKKROSEFKLOEELNKVGLIK 242
 Db 653 KLEDEMAAKAGELIRLRISQINSVK--AAVEDEKAVVAGEK 690

RESULT 13

S04090

myosin heavy chain 3, skeletal muscle, embryonic - human

N:Contains: myosin ATPase (EC 3.6.4.1)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002

C:Accession: S04090; S06146; S05442; S12460; S09333; A35082

R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Rubinstein, N.A.; Kelly, A.M.

Nucleic Acids Res. 17, 3591-3592, 1989

A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.

A:Reference number: S04090; PMID:89263803; PMID:2726495

A:Accession: S04090

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-1940 <EL>

R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Wu, Q.L.; Raychowdhury, M.K.

FEBS Lett. 256, 21-28, 1989

A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation

A:Reference number: S06146; PMID:90033298; PMID:2806546

A:Accession: S06146

A:Molecule type: mRNA

A:Residues: 774-1662, 'GT', 1665-1940 <EL>

A:Cross-references: EMBL:X13100; NID:931143; PIDN:CAA31492.1; PID:931144

R:Karsch-Mizrachi, I.; Travis, M.; Blau, H.; Levinand, L.A.

Nucleic Acids Res. 17, 6167-6179, 1989

A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle my

A:Reference number: S05442; PMID:8936668; PMID:2771643

A:Accession: S05442

A:Molecule type: DNA

A:Residues: 856-1390, 'KK', 1393-1940 <KAR>

A:Cross-references: EMBL:X15696; NID:936504; PIDN:CAA33731.1; PID:91335313

R:Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.

J. Biol. Chem. 265, 3568-3576, 1990

A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals e

A:Reference number: A35082; PMID:90154023; PMID:2303463

A:Contents: annotation; chromosomal assignment

R:Bober, E.

submitted to the EMBL Data Library, January 1989

A:Reference number: S12458

A:Accession: S12460

A:Molecule type: mRNA

A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>

A:Cross-references: EMBL:X51593; NID:929463; PIDN:CAA35942.1; PID:929464

R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.

Eur. J. Biochem. 189, 55-65, 1990

A:Title: Identification of three developmentally controlled isoforms of human myosin

A:Reference number: S09333; PMID:90235862; PMID:1691980

A:Accession: S09333

A:Molecule type: mRNA

A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-125

1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOB>

A:Cross-references: EMBL:X51593

C:Genetics:

A:Gene: GDB:MW3

A:Cross-references: GDB:119443; OMIM:160720

A:Map position: 17p13.1-17p13.1

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; muscle

F:89-767/Domain: myosin motor domain homology <MOT>

F:179-186/Region: nucleotide-binding motif A (P-loop)

F:549-586/Region: actin binding #status predicted

F:656-678/Region: actin binding #status predicted

F:840-1280/Domain: coiled coil #status predicted <COI>

F:840-1280/Region: S2

F:1281-1940/Region: light meromyosin

F:130/Modified site: N6, N6-trimethyllysine (lys) #status predicted

F:185/Binding site: ATP (lys) #status predicted

F:996/706/Active site: Cys #status predicted

Query Match

Best Local Similarity 14.9%; Score 178.5; DB 1; Length 1940;

Matches 68; Conservative 62; Mismatches 105; Indels 121; Gaps 7;

QY 8 VQSLDEVTAQFESYKALTFSETEDEKLENSLOEKAKKNAEDVOHOIATFESSNOY 67
 Db 1208 IDNLQVOKOKLEKSEFKLETDIDSSMSVSKSANLEKICRTLEDLSPARGKNEI 1267
 QY 68 VMMLDLQTKSALKETEKEIT-----VSFLQKITDLONOLOKQOED- 109
 Db 1268 QSLSELTLQKRLQTEAGELSRQLEKESIVSQLSRSQAFTQQTTELKRLDEENKAK 1327
 QY 110 -----FKQLDEGRKAKEKNTTALTEINKMRLYE----- 143
 Db 1328 NALNALQSSRDHCDLLRQVDEEGKAELOALSKANSSEVAQWRKYETDAIORTTEL 1387
 QY 144 -----ELYN-----KTK----- 150
 Db 1388 EAAQELQALQDQSEQVAVNAKASLEKTKORLQGEVEDLMVDVERANSLLAALDKQ 1447

OY 151 -----PFOIOLAFEFEXKQALLNENGAQOINKIRDSYAKILG-----HONIK 194
 Db 1448 RNFQVLAWKTCKECSQSLKESKSTELSTELKNAEALDQETVREKKNLE 1507
 OY 195 QRIKHVVKLDKENSQKSEVSKRLRCQLAKK-----QSEFKLOEELNKVGIK 242
 Db 1508 QEIADLTQEIANGKTIHLEKSRKQIELEKADIQALAEFALEHAEKILIRIO 1563
 RESULT 14
 JX0178
 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken
 N:Contains: myosin ATPase (EC 3.6.4.1)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Apr-2002
 C:Accession: PX0050; PX0051; JX0178; A26365; S02082; PM0009; S39081; S24351; S05
 R:Hayashida, M.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 54-59, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the
 A:Reference number: PX0050; MUID:92041767; PMID:1939027
 A:Accession: PX0050
 A:Molecule type: protein
 A:Residues: 1-205 <HAY>
 R:Komine, Y.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 60-67, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of th
 A:Reference number: PX0051; MUID:92041768; PMID:1939028
 A:Accession: PX0051
 A:Molecule type: protein
 A:Residues: 206-636 <KOM>
 R:Maita, T.; Miyamishi, T.; Matsuzono, K.; Tanioka, Y.; Matsuda, G.
 J. Biochem. 110, 68-74, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of t
 A:Reference number: PX0052; MUID:92041769; PMID:1939029
 A:Accession: PX0052
 A:Molecule type: protein
 A:Residues: 201-213; 632-837 <MAT>
 R:Maita, T.; Yajima, E.; Nagata, S.; Miyamishi, T.; Nakayama, S.; Matsuda, G.
 J. Biochem. 110, 75-87, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of th
 A:Reference number: JX0178; MUID:92041770; PMID:1939030
 A:Accession: JX0178
 A:Molecule type: protein
 A:Residues: 833-1938 <MA2>
 R:Maita, T.; Hayashida, M.; Tanioka, Y.; Komine, Y.; Matsuda, G.
 Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987
 A>Title: The primary structure of the myosin head
 A:Reference number: A26365; MUID:87092420; PMID:3467365
 A:Accession: A26365
 A:Molecule type: protein
 A:Residues: 1-129, 'X', 131-139, 141-550, 'X', 552-754, 'X', 756-784, 'QL', 787-804, 806-810 <MA3>
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 55-61, 1989
 A>Title: Amino acid sequence of the hinge region in chicken myosin subfragment-2.
 A:Reference number: S02082; MUID:89228549; PMID:2713098
 A:Accession: S02082
 A:Molecule type: protein
 A:Residues: 1144-1270 <MAT>
 R:Yajima, E.
 Nagasaki Igakkai Zasshi 65, 409-430, 1990
 A>Title: Study on tail region of skeletal muscle myosin: primary structure and protease
 A:Reference number: PM0009
 A:Accession: PM0009
 A:Molecule type: protein
 A:Residues: 1304-1938 <YAJ>
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 Submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization of
 A:Reference number: S39081
 A:Accession: S39081
 A:Molecule type: mRNA
 A:Residues: 1081-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1795, 'HV', 1798-1829, 'S', 1831
 A:Cross-references: EMBL:M74084

R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A>Title: Analysis of the chicken fast myosin heavy chain family. Localization of isofo
 A:Reference number: S24348; MUID:92309413; PMID:1377278
 A:Accession: S24351
 A:Molecule type: mRNA
 A:Residues: 1082-1182, 'T', 1184-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1780, 'M', 17
 A:Cross-references: EMBL:M74084
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 1027-1034, 1989
 A>Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal musc
 A:Reference number: S05515; MUID:90121764; PMID:2610940
 A:Accession: S05515
 A:Molecule type: protein
 A:Residues: 842-906, 'Q', 908-1270 <MA3>
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 549-558, 1989
 A>Title: Amino acid sequence of the short subfragment-2 in adult chicken skeletal mus
 A:Reference number: S04501; MUID:89374803; PMID:2775482
 A:Accession: S04501
 A:Molecule type: protein
 A:Residues: 852-906, 'Q', 908-1108 <MA2>
 R:Matsuda, G.; Maita, T.; Miyamishi, T.; Hayashida, M.
 J. Protein Chem. 6, 33-46, 1987
 A>Title: Structure and function of muscle myosin.
 A:Reference number: A60877
 A:Accession: A60877
 A:Molecule type: protein
 A:Residues: 1-139, 141-205 <MA1>
 R:Gulick, J.; Kropp, K.; Robbins, J.
 J. Biol. Chem. 260, 14513-14520, 1985
 A>Title: The structure of two fast-white myosin heavy chain promoters. A comparative
 A:Reference number: A92507; MUID:86033956; PMID:2997212
 A:Accession: A24124
 A:Molecule type: DNA
 A:Residues: 'M', 1-168 <GU1>
 A:Cross-references: GB:M13512; GB:M12083; GB:M13510; NID:g212363; PIDN:AAA48966.1; PI
 R:Kropp, K.; Gulick, J.; Robbins, J.
 J. Biol. Chem. 261, 6613-6618, 1986
 A>Title: A canonical sequence organization at the 5'-end of the myosin heavy chain ge
 A:Reference number: A92587; MUID:86196091; PMID:3009465
 A:Accession: C25217
 A:Molecule type: DNA
 A:Residues: 'M', 1-56, 'T', 58-76, 'T', 78-168 <KRO>
 A:Cross-references: GB:M13515; GB:M13511; NID:g212373; PIDN:AAA48971.1; PID:g555468
 C:Comment: This is a fragment of the globular head.
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methyl
 F:1-1938/Product: myosin heavy chain #status experimental <MAT>
 F:89-768/Domain: nucleotide-binding motif A (P-loop)
 F:179-186/Region: nucleotide-binding motif A (P-loop)
 F:550-587/Region: actin binding #status predicted
 F:657-679/Region: actin binding #status predicted
 F:841-1938/Domain: coiled coil <CO1>
 F:841-1289/Region: S2
 F:852-1108/Domain: short subfragment 2 <SUB2>
 F:1290-1938/Region: light meromyosin
 F:1/Modified site: acetylated amino end (Ala) #status experimental
 F:35/Modified site: N6-methyllysine (Lys) #status experimental
 F:130-551/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
 F:185/Binding site: ATP (Lys) #status predicted
 F:697-707/Active site: Cys #status predicted
 F:755/Modified site: 3'-methylhistidine (His) #status experimental
 Query Match 14.9%; Score 177.5; DB 1; Length 1938;
 Best Local Similarity 20.5%; Pred. NO. 0.11;
 Matches 73; Conservative 55; Mismatches 107; Indels 121; Gaps 10;
 OY 8 VOSLEDVYNAOFESYVALALASEEDIKLNNSSIOEKAARAGNAEVOHIOIATSESSNOEY 67
 Db 1209 IDNLORVQKLEKEKSELKEMIDLASWESKAKANLEKWCRTLEOLSEIKREBON 1268
 OY 68 VRMLDLOTKSALKETEI-----KEITVS-----FLQKITDLOQLKQO----- 106


```
Db      1269 ORMIINDLMTQRLQETGEGYSROAEKEDKALISLGRKOGFTQOIEELKRLHEEIKAK 1328
OY      107 -----EED---FRKOLEDEGRKAKENTTAELLTEINKRRLY-----EEL 145
Db      1329 NALAHALQSRHODDLREYEEBQEKGLQALSKANSEVAQWRTKYETDAIQRTIEL 1388
OY      146 YNKTKEPQIOLD-----AFEEVKQALLNE-----HGAQEQUNKIR 181
Db      1389 EEAKKKLAQRLQDAEEHVAVNAKASLEKTKQRLQNEVEDLMVDVERSNACALDKKQ 1448
OY      182 DSYAKLIGHQNIK-----OKIKHYVTKLDENSOLK 211
Db      1449 KNFDKTLAEKKQKEETQTELEASQKESRSLSTELFKMKNAYEESLDHETLKRKNKQ 1508
OY      212 SEVSKLRQOLA-----K-----KQSETKLOELNKVLGIR 242
Db      1509 QETADLTQALAEGSKAVHELEKVKKHVEQKSELQALAEASLSHEECKILRLQ 1564
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RESULT 15

148176

synaptonemal complex protein - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence-revision 02-Jul-1996 #text-change 05-Nov-1999

C:Accession: 148176

R:Dobson, M.J.; Pearlman, R.E.; Karaiskakis, A.; Spyropoulos, B.; Moens, P.B.

J. Cell Sci. 107, 2749-2760, 1994

A:Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disj

A:Reference number: 148176; MUID:95181577; PMID:7876343

A:Accession: 148176

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-845 <RES>

A:Cross-references: GB:L32978; NID:9598124; PIDN:AAC42039.1; PID:9598125

C:Genetics:

A:Gene: syn1

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Query Match      14.88; Score 176.5; DB 2; Length 845;
Best Local Similarity 23.18; Pred. No. 0.054;
Matches 79; Conservative 55; Mismatches 97; Indels 111; Gaps 14;
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```
OY      5 DSMVQSLQEDVTAQPESEYKALTASIEDLKLKLENSLQ-EKAAK--AGKNAE----- 51
Db      273 DEMTKFKNNNEVKLELKLTLA---EDQKLDEKKQVEKLAELQCKEQELTLLQTRK 329
OY      52 ---DVQHQLATSSNQEVVRLMLDQTKSALKETEIK--ETVS-----FLQKI 96
Db      330 EVHDLERQLLVTKISDQNSKYQVEELKTK--LEBEKLNKMLTASCGKLSLENNKLTQET 387
OY      97 TDLQNL-----KQOEDPRKQLEDEGR----- 120
Db      388 NDMALELKQYQEDITNSKQOERMLQIENLEKEKHLRDELSVREKFIQOGNEVCKL 447
OY      121 -----KAEK-----ENTTALTEINKMRLYLELYNKTKEPQ----- 153
Db      448 DKSEENARSTIECEVLLKKEQMKILEKCNLKRQAEKSKYIEELHGENKALKKKSSAES 507
OY      154 IOLDAFEVERQALLNEHGAQEQUNKIRDSY-----AKLLGHONLKQIKHVVYKLDENS 208
Db      508 KQINAYEIKVKNKIQLELESARKQFOEWTQYQKEIEVKRISBEKLLGEVEKAKAMVDEAV 567
OY      209 QLKSEVSKLRQO-----LAKKQSETKLOELNKVIGI 241
Db      568 KLDQREID-LRQQRKIAEMVALMEKHQYQKIVEERDSELGL 608
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Search completed: July 17, 2003, 16:11:17
Job time : 20 secs